A novel bacterial flavoenzyme (BVMO) for biotechnological applications

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Baeyer-Villiger monooxygenases (BVMOs) are flavin-containing enzymes that catalyse a wide variety of oxidative reactions specifically on the carbonyl moiety of substrates, many of which are difficult to achieve using chemical approaches. Moreover, these proteins have great value in the areas of bioremediation and green chemistry.

A novel BVMO gene in *Acinetobacter radioresistens* S13 was identified and using Clustal V its amino acid sequence was aligned with known BVMOs. Phylogenetic analysis demonstrated that it clustered together with BVMO from Mycobacterium, distant from the classical cycloalkanone MOs.

After cloning and successful expression in *E.coli*, the BVMO protein was purified in high yields (20mg/L culture) using Nickel affinity chromatography. Preliminary characterisation showed a 57 kDa soluble protein with a tightly but non-covalently bound FAD. Due to the large substrate specificity of BVMOs, a 3D homology model of this enzyme was generated in order to select its putative substrates using *in silico* docking. Well-defined substrate profiles are available for several BVMOs and together with our model this may allow careful predictions for substrates of this novel enzyme.